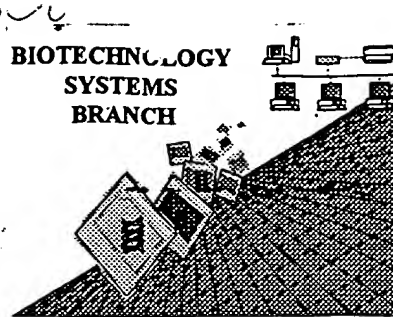


RAW SEQUENCE LISTING
ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/717,883

Source: OIPE

Date Processed by STIC: 12/7/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/712,883

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 Wrapped Aminos The amino acid-number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 Variable Length Sequence(s) contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 Use of <213> Organism (NEW RULES) Sequence(s) are missing this mandatory field or its response.
- 12 Use of <220> Feature (NEW RULES) Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/717,883

DATE: 12/07/2000
 TIME: 12:44:33

Input Set : A:\Dex-0115.app
 Output Set: N:\CRF3\12072000\I717883.raw

Does Not Comply
 Corrected Diskette Needed

3 <110> APPLICANT: Salceda, Susana
 4 Cafferkey, Robert
 5 Lou, Xing Jian
 6 Recipon, Herve
 7 Sun, Yongming
 9 <120> TITLE OF INVENTION: A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING,
 10 IMAGING AND TREATING CANCER
 12 <130> FILE REFERENCE: DEX-0115
 14 <140> CURRENT APPLICATION NUMBER: US/09/717,883
 15 <141> CURRENT FILING DATE: 2000-11-21
 17 <150> PRIOR APPLICATION NUMBER: 60/166,818
 18 <151> PRIOR FILING DATE: 1999-11-22
 20 <160> NUMBER OF SEQ ID NOS: 4
 22 <170> SOFTWARE: PatentIn Ver. 2.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1635
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapiens
 29 <400> SEQUENCE: 1
 30 tcgcggcgccg agggagccggc gccggggcgcc tggggagggc ttgctgacgc tgcggggccaa 60
 31 gccgccctcg gaggccaggt acaccgacgt gctgcagaag atcaagtaag ccttcaagcct 120
 32 gctgggcccg ctgcgcggca acatcgccga cccctcctct ccggagctgt tgcacttccr 180
 33 ttccgggccc ctgcagatga ttgtgaacac gtcggggggg ccggagttcg cgagcagtg 240
 34 gcggcgcccg catctgacat cggatgccgt ggcgctgctg cgggacaacg tcaactccacg 300
 35 tgaaaacgag ctctggacct cgttggggga ctcttgagcc cggcccgggc tggagctgtc 360
 36 cccygagagg ygaaccccat acagaccgga gttcttcagc ggctgggagc cgcgggtcac 420
 37 tgacccgcag agccgcgcct yggaggaccc agttgagaaa cagctacagc acgagcgag 480
 38 gcgcgcgcag caaagcgccc ccgaggtcgc tgtcaalggc caccgaggac ttggggagcca 540
 39 gaactctgag ctacagctga gtcagagaca gcaggaaaat gggtcctgtg taattatgac 600
 40 ttccaggccc gcaacagcag tgagctgtcg gtcaagcagc gggacgtact ggaggtcctg 660
 41 gatgacagtc gtaagtgtg yaaagttcgg gacccagcgg ggcaggaggg atatgtgcc 720
 42 tacaacatcc tgacacctta ccccggaacc cggctgcacc acagccaaag ccccgcccg 780
 43 agcctgaaca gcaactcctc tccaccacca gccccagccc cgggccacc tccagctctg 840
 W--> 44 gctcgcccc gctgggacag gcccgctgg gacagctgcg atantcaac ggcttgagc 900
 45 ccagcgaga ggaataatc tcccaagatc tcatcgtaa cgaaggaact caggcgccg 960
 46 tggcccgagg ccgctcgga ccgagcccg caytcccagg gcccccgccc ccggaaccg 1020
 W--> 47 agctcagccc gggctcggac gccctcggag tccgcgcctg gctgcagcnc aagggttta 1080
 48 gctccgggac cgtggagcgg ctgggtgtgc tgaccggggc gcacttttct cgtgcagaa 1140
 49 agaggagctg cgggcygtga gccccgagga gggggcacgt ggttacagcc aggtcacct 1200
 50 gcagcgcttc gctgctggag gacaaagaga aagtgtcaga gctggaggca gtgatggaga 1260
 51 agcaaaagaa gaaggtggaa ggcgaggtgg aaatggaggt catltgacct gccagggcc 1320
 52 ctlcgcaaa agtgacgagg ccccgctggg gaacggactc ctacagctct ccccaatagc 1380
 53 ggaagtcgat cttctgaagg atggcraatc tgcctcgccc ctgggtcttc cccatcccg 1440
 54 tggacagact taacgatcct tgctgcagtc cctccggaga ggaatctggac tggctgggag 1500
 55 tggggagggc gtggagacag tctacggaaa gcyctagcag acccccgaga ggtgacagtg 1560
 56 gagccctgag catlgtataa tgcgggcccg cctataaaca gcttcctgtc ttaycagatg 1620
 W--> 57 gtgtgccant thaaa 1635

see item 10
 on Ena Summary
 sheet

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/717,883

DATE: 12/07/2000
TIME: 12:44:33

Input Set : A:\Dex-0115.app
Output Set: N:\CRF3\12072000\I717883.raw

60 <210> SEQ ID NO: 2
61 <211> LENGTH: 21
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
68 <400> SEQUENCE: 2
69 cccaatagcg gaaatcgatc t 21
72 <210> SEQ ID NO: 3
73 <211> LENGTH: 20
74 <212> TYPE: DNA
75 <213> ORGANISM: Artificial Sequence
77 <220> FEATURE:
78 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
80 <400> SEQUENCE: 3
81 cactcccagc cagtccagat 20
84 <210> SEQ ID NO: 4
85 <211> LENGTH: 22
86 <212> TYPE: DNA
87 <213> ORGANISM: Artificial Sequence
89 <220> FEATURE:
90 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
92 <400> SEQUENCE: 4
93 aatctgctcc ggcctggtc tt 22

VERIFICATION SUMMARY DATE: 12/7/2000
PATENT APPLICATION: US/09/717,883 TIME: 12:44:34

Input Set : A:\Dex-0115.app
Output Set: N:\CRF3\12072000\I717883.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:44 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:44 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
L:44 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:47 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1
M:340 Repeated in SeqNO=1
L:57 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:1
L:57 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:1
L:57 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:1
L:57 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1